

5'	GGG	ACT	TCC	AGT	AGG	CGG	CAT	GTT	TGA	AAA	GTG	ATG	ACG	GTT	GAC	GTT	TGC	54	
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
	63		72		72		81		81		90		90		99		99		108
	TGA	TTT	TTG	ACT	TTG	CTT	GTA	GCT	CCC	CGA	ACT	CGC	CGT	CTT	CCT	GTC	GTC	GTC	
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
	117		126		126		135		135		144		144		153		153		162
	GCG	CGG	CAC	TGT	AGG	TGA	GCG	CGA	GAG	GAC	GGA	AGG	AAG	CCT	GCA	GAC	GAC	AGA	
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
	171		180		180		189		189		198		198		207		207		216
	CGC	CTT	CTC	CAT	CCC	AAG	GCG	CGG	GCA	GCG	GCC	GGG	ACG	CTG	GGC	CTG	GCG	CTG	
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
	225		234		234		243		243		252		252		261		261		270
	TAA	TCG	TGC	TCA	GCG	GTG	GGA	GGA	GGA	GGA	GGA	AGA	AAC	CAG	AGC	CTG	GGA	GAT	
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
	279		288		288		297		297		306		306		315		315		324
	TAA	CAG	GAA	ACT	TCC	AAG	ATG	GAA	ACT	TTG	TCT	TTC	CCC	AGA	TAT	AAT	GTA	GCT	
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
				M	E	T	L	S	F	P	R	Y	N	V	A				
	333		342		342		351		351		360		360		369		369		378
	E	I	V	I	H	I	R	N	K	I	L	T	G	A	D	G	K	N	

FIGURE 1A

387	396	405	414	423	432
CTC	ACC	AAG	AAT	GAT	CTT
T	T	K	N	D	L
441	450	459	468	477	486
TAC	ATG	AGA	GCC	TTA	CAA
Y	M	R	A	L	Q
495	504	513	522	531	540
ATG	CCA	GTG	AAC	TCT	GAA
M	P	V	N	S	E
549	558	567	576	585	594
TTC	AGC	AAT	TTA	GTT	ACT
F	S	N	L	V	T
603	612	621	630	639	648
GAC	TTT	GAG	ACT	GCT	GAT
D	F	E	T	A	D
657	666	675	684	693	702
TTA	AGT	GGC	ATT	ATC	AAC
L	S	G	I	I	N

FIGURE 1B

ATG	GAA	711	720	TGG	CAA	TAT	AAA	TCC	TCT	GCG	GAC	AAA	ATG	CAA	CAG	TTA	AAC
M	E	F	L	W	Q	Y	K	S	S	A	D	K	M	Q	Q	L	N
GCC	GCA	765	774	GAG	GCA	TTA	ATG	AAA	CTG	GAG	AGA	CTT	GAT	TCT	GTT	CCA	GTT
A	A	H	Q	E	A	L	M	K	L	E	R	L	D	S	V	P	
GAA	GAG	819	828	GAA	GAG	TTC	AAG	CAG	CTT	TCA	GAT	GGA	ATT	CAG	GAG	CTA	CAA
E	E	Q	E	E	F	K	Q	L	S	D	G	I	Q	E	L	Q	Q
TCA	CTA	873	882	CAG	GAT	TTT	CAT	CAA	AAA	ACG	ATA	GTG	CTG	CAA	GAG	GGA	AAT
S	L	N	Q	D	F	H	Q	K	T	I	V	L	Q	E	G	N	S
CAA	AAG	927	936	TCA	AAT	ATT	TCA	GAG	AAA	ACC	AAG	CGT	TTG	AAT	GAA	CTA	AAA
Q	K	K	S	N	I	S	E	K	T	K	R	L	N	E	L	K	L
TCG	GTG	981	990	AAA	GAA	ATA	CAA	GAG	AGT	TTG	AAA	ACA	AAA	ATT	GTG	GAT	
S	V	V	S	L	K	E	I	Q	E	S	L	K	T	K	I	V	D

FIGURE 1C

TCT	CCA	GAG	AAG	TTA	AAG	AAT	TAT	AAA	GAA	AAA	ATG	AAA	GAT	ACG	GTC	CAG	AAG
S	P	E	K	L	K	N	Y	K	E	K	M	K	D	T	V	Q	K
1035	1044	1053	1062	1071	1080												
CTT	AAA	AAT	GCC	AGA	CAA	GAA	GTG	GTG	GAG	AAA	TAT	GAA	ATC	TAT	GGA	GAC	TCA
L	K	N	A	R	Q	E	V	V	E	K	Y	E	I	Y	G	D	S
1089	1098	1107	1116	1125	1134												
GTT	GAC	TGC	CTG	CCT	TCA	TGT	CAG	TTG	GAA	GTG	CAG	TTA	TAT	CAA	AAG	AAC	TCA
V	D	C	L	P	S	C	Q	L	E	V	Q	L	Y	Q	K	K	I
1143	1152	1161	1170	1179	1188												
CAG	GAC	CTT	TCA	GAT	AAT	AGG	GAA	AAA	TTA	GCC	AGT	ATC	TTA	AAG	GAG	AGC	ATA
Q	D	L	S	D	N	R	E	K	L	A	S	I	L	K	E	S	L
1197	1206	1215	1224	1233	1242												
AAC	TTG	GAG	GAC	CAA	ATT	GAG	AGT	GAT	GAG	TCA	GAA	CTG	AAG	AAG	GAG	AGC	CTG
N	L	E	D	Q	I	E	S	D	E	S	E	L	K	K	L	K	T
1251	1260	1269	1278	1287	1296												
GAA	GAA	AAT	TCG	TTC	AAA	AGA	CTG	ATG	ATT	GTG	AAG	AAG	GAA	AAA	CTT	GCC	ACA
E	E	N	S	F	K	R	L	M	I	V	K	K	E	K	L	A	T
1305	1314	1323	1332	1341	1350												

FIGURE 1D

GCA	CAA	TTC	AAA	ATA	AAT	AAG	CAT	GAA	GAT	GTT	AAG	CAA	TAC	AAA	CGC	ACA	
A	Q	F	K	I	N	K	K	H	E	D	V	K	Q	Y	K	T	
V	I	E	D	C	N	K	V	Q	E	K	R	G	A	V	Y	E	
GTA	ATT	GAG	GAT	TGC	AAT	AAA	GTT	CAA	GAA	AAA	AGA	GGT	GCT	TAT	GAA	CGA	
V	I	E	D	C	N	K	V	Q	E	K	R	G	A	V	Y	E	
GTA	ACC	ACA	ATT	AAT	CAA	GAA	ATC	CAA	AAA	ATT	AAA	CTT	GGA	ATT	CAA	CAA	CTA
V	T	T	I	N	Q	E	I	Q	K	I	K	L	G	I	Q	L	
AAA	GAT	GCT	GCT	GAA	AGG	GAG	AAA	CTG	AAG	TCC	CAG	GAA	ATA	TTT	CTA	AAC	TTG
K	D	A	A	E	R	E	K	L	K	S	Q	E	I	F	L	N	L
AAA	ACT	GCT	TTG	GAG	AAA	TAC	CAC	GAC	GGT	ATT	GAA	AAG	GCA	GAG	GAC	TCC	
K	T	A	L	E	K	Y	H	D	G	I	E	K	A	A	E	D	S
TAT	GCT	AAG	ATA	GAT	GAG	AAG	ACA	GCT	GAA	CTG	AAG	AGG	AAG	ATG	TTC	AAA	ATG
Y	A	K	I	D	E	K	T	A	E	L	K	R	K	M	F	K	M

FIGURE 1E

FIGURE 1F

1	M E T I L S F P R Y N V A E I V I H I R N K I L T G A D G K N	GRIIP
1	M E T I L S F P R Y N T A E I V V H I R N K L L T G A D G K N	HW051
31	L T K N D L Y P N P K P E V L H M I Y M R A L Q I V Y G I R	GRIIP
31	L S K S D F L P N P K P E V L Y M I Y M R A L Q I V Y G I R	HW051
61	L E H F Y M M P V N S E V M Y P H L M E G F L P F S N L V T	GRIIP
61	L E H F Y M M P V N I E V M Y P H T M E G F L P V S N L F F	HW051
91	H L D S F L P I C R V N D F E T A D I L C P K A K R T S R F	GRIIP
91	H L D S F M P I C R V N D F E T A D I L C P K A K R T S R F	HW051
121	L S G I I N F I H F R E A C R E T Y M E F L W Q Y K S S A D	GRIIP
121	L S G I I N F I H F R E T C L E K Y E E F L L Q N K S S V D	HW051
151	K M Q Q L N A A H Q E A L M K L E R L D S V P V E E Q E E F	GRIIP
151	K I Q Q L S N A H Q E A L M K L E K L N S V P V E E Q E E F	HW051
181	K Q L S D G I Q E L Q Q S L N Q D F H Q K T I V L Q E G N S	GRIIP
181	K Q L K D D I Q E L Q H L L N Q D F R Q K T T L L Q E R Y T	HW051
211	Q K K S N I S E K T K R L N E L K L S V V S L K E I Q E S L	GRIIP
211	K M K S D F S E K T K H V N E L K L S V V S L K E V Q D S L	HW051

FIGURE 2A

241	K T K I V D S P E K L K N Y K E K M K D T V Q K L K N A R Q	GRITP
241	K S K I V D S P E K L K N Y K E K M K D T V Q K L K R S A R E	HW051
271	E V V E K Y E I Y G D S V D C L P S C Q L E V Q L Y Q K K I	GRITP
271	E V M E K Y D I Y R D S V D C L P S C Q L E V Q L Y Q K K S	HW051
301	Q D L S D N R E K L A S I L K E S L N I E D Q I E S D E S E	GRITP
301	Q D L A D N R E K L S S I L K E S L N I E G Q I D S D S S E	HW051
331	L K K L K T E E N S F K R L M I V K K E K L A T A Q F K I N	GRITP
331	L K K L K T E E N S L I R L M T L K K E R L A T M Q F K I N	HW051
361	K K H E D V K Q Y K R T V I E D C N K V Q E K R G A V Y E R	GRITP
361	K K Q E D V K Q Y K R T M I E D C N K V Q E K R D A V C E Q	HW051
391	V T T I N Q E I Q K I K L G I Q Q L K D A A E R E K L K S Q	GRITP
391	V T A I N Q D I H K I K S G I Q Q L R D A E K R E K L K S Q	HW051
421	E I F L N L K T A L E K Y H D G I E K A A E D S Y A K I D E	GRITP
421	E I L V D L K S A L E K Y H E G I E K T T E E C C T R I L G G	HW051
451	K T A E L K R K M F K M S T	
451	K T A E L K R R M F K M P P	

FIGURE 2B

Tissue Category	Clone Count	Found in	Ab Abund	Pct Abund
Cardiovascular System	266190	4/68	4	0.0015
Connective Tissue	144645	1/47	2	0.0014
Digestive System	501101	3/148	4	0.0008
Embryonic Structures	106713	2/21	2	0.0019
Endocrine System	225386	1/53	1	0.0004
Exocrine Glands	254635	2/64	2	0.0008
Genitalia, Female	427284	3/106	3	0.0007
Genitalia, Male	448207	2/114	6	0.0013
Germ Cells	38282	1/5	1	0.0026
Hemic and Immune System	680277	15/159	20	0.0029
Liver	109378	0/35	0	0.0000
Musculoskeletal System	159280	0/47	0	0.0000
Nervous System	955753	2/19	2	0.0002
Pancreas	110207	1/24	1	0.0009
Respiratory System	390086	4/93	5	0.0013
Sense Organs	192256	1/8	1	0.0052
Skin	722292	0/15	0	0.0000
Stomatognathic System	12923	0/10	0	0.0000
Unclassified/Mixed	120926	3/13	5	0.0041
Urinary Tract	279062	2/64	2	0.0007
Totals	5321883	47/1292	6	0.0000

FIGURE 3A

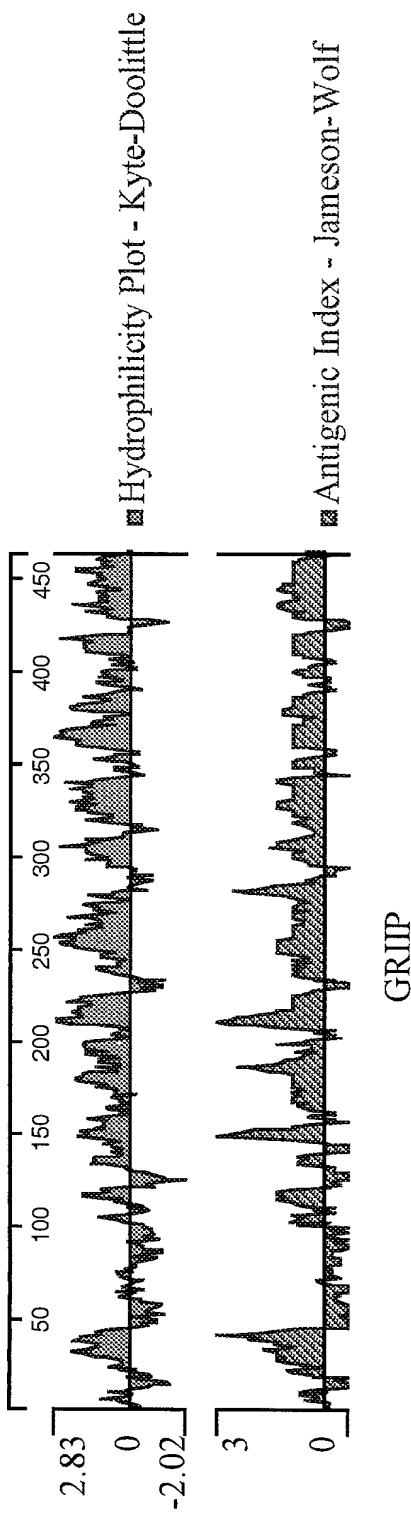
Found in:

Library ID	Clone Count	Library Description	Abund	Pct Abund
BMARTXR02	682	bone marrow tumor line, neuroblastoma, t/6-OHDA,	1	0.1466
TLYMUNTO1	3669	T-lymphocytes, allogenic, 40-50M, untreated	3	0.0818
TBLMNTO1	3119	T-B lymphoblast line, leukemia, untreated	2	0.0641
U937NOT01	2067	monocyte line, histiocytic lymphoma, untreated	1	0.0484
BMARTXT03	2162	bone marrow tumor line, neuroblastoma, t/6-OHDA	1	0.0463
BMARTXT06	2787	bone marrow tumor line, neuroblastoma, untreated	1	0.0359
SPLNTUT02	3017	spleen tumor, Hodgkin's, 45M	1	0.0331
MCLDTXT04	3310	UCB, derived dendritic cells, t/PMA, Ionomycin	1	0.0302
THYMFET03	3577	thymus, fetal, M	1	0.0280
MYEPTXT01	3944	CML precursor line, K-562, 53F, t/5AZA 72 h	1	0.0254
SPLNFET02	7859	spleen, fetal, 23M	1	0.0127
TLYMNOT08	9784	T-lymphocytes, allogenic anergic, t/OKT3 3 day	1	0.0102

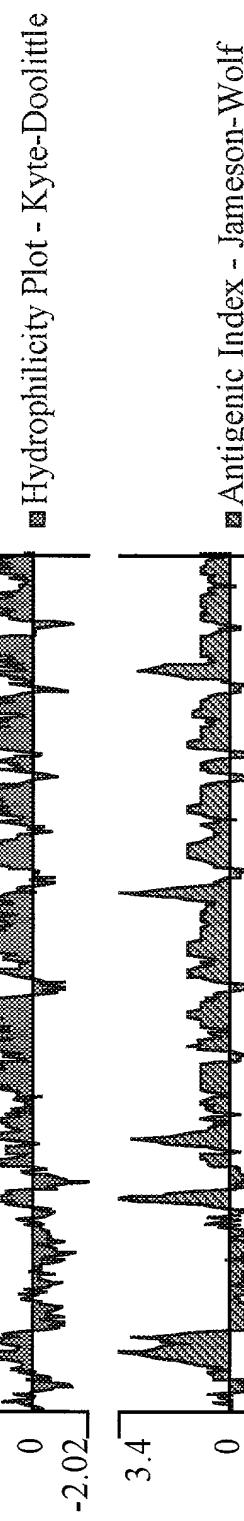
Two pooled libraries, two normalized libraries, and one subtracted library are not shown.

FIGURE 3B

Hydrophilicity Plot - Kyte-Doolittle



GRIP



HW051

FIGURE 4